

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 20:58:41 ; Search time 1527.5 Seconds
(without alignments)
16168.980 Million cell updates/sec

Title: US-10-025-514-7

Perfect score: 1525

Sequence: 1 tctagaccatgctgaaag.....ccaactcagaagtagtcgac 1525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	433.2	28.4	2478	11	AF130068
2	431.6	28.3	2571	11	AF113676
3	331.6	21.7	1392	11	AK002537
4	318.8	20.9	1296	11	AK004999
5	309.8	20.3	887	14	BQ643710
6	305.4	20.0	907	14	BQ648909

7	289.6	19.0	895	14	BQ653587	AGENCOURT
8	287	18.8	985	14	BM924019	AGENCOURT
9	285.2	18.7	924	14	BQ646142	AGENCOURT
10	283.8	18.6	924	14	BQ958958	AGENCOURT
11	274.8	18.0	1194	14	BM924813	AGENCOURT
12	273.4	17.9	907	14	BQ650189	AGENCOURT
13	271.4	17.8	891	14	BQ646948	AGENCOURT
14	270.4	17.7	959	14	BQ648524	AGENCOURT
15	268	17.6	796	12	BQ567260	AGENCOURT
16	264.8	17.4	833	14	BQ007663	UI-H-EIO-
17	264.8	17.4	991	14	BQ064738	AGENCOURT
18	263.8	17.3	917	14	BQ650502	AGENCOURT
19	263.6	17.3	687	10	AV649258	AV649258
20	263	17.2	916	14	BQ644130	AGENCOURT
21	262	17.2	686	12	BQ569467	AGENCOURT
22	261	17.1	1012	14	BQ064473	AGENCOURT
23	260.2	17.1	977	14	BQ654015	AGENCOURT
24	259.6	17.0	740	10	AV653778	AV653778
25	256.6	17.0	944	14	BQ645533	AGENCOURT
26	256	16.8	869	13	BI219058	AGENCOURT
27	254	16.7	917	14	BQ650698	AGENCOURT
28	253	16.6	654	12	BQ563537	AGENCOURT
29	251.4	16.5	884	12	BQ536548	AGENCOURT
30	250.6	16.4	746	12	BQ566873	AGENCOURT
31	250.2	16.4	745	9	AI114643	AI114643
32	249.8	16.4	1044	9	AI528087	AI528087
33	249.6	16.4	813	13	BI759000	BI759000
34	249.4	16.4	764	12	BF384318	BF384318
35	249	16.3	731	10	AV649144	AV649144
36	248.8	16.3	804	12	BG618951	BG618951
37	247.4	16.2	813	14	BQ182052	BQ182052
38	245.8	16.1	780	9	AI110706	AI110706
39	244.2	16.0	992	13	BI246204	BI246204
40	243.8	16.0	752	12	BG618001	BG618001
41	243.2	15.9	674	14	BM724546	BM724546
42	243.2	15.9	759	12	BG533293	BG533293
43	243	15.9	749	9	AT526727	AT526727
44	242.8	15.9	790	13	BI761275	BI761275
45	242.6	15.9	934	14	BQ646994	BQ646994

ALIGNMENTS

RESULT 1
AF130068
LOCUS Homo sapiens clone FLB8226 PRO2209 mRNA, complete cds.
DEFINITION Homo sapiens clone FLB8226 PRO2209 mRNA, complete cds.
ACCESSION AF130068
VERSION AF130068.1 GI:11493442
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2478)
AUTHORS Zhang,C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y., Xu,W., Gao,F., Liu,M. and He,F.
TITLE Functional prediction of the coding sequences of 75 new genes deduced by analysis of cDNA clones from human fetal liver
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2478)
AUTHORS Zhang,C., Yu,Y., Zhang,S., Wei,H., Bi,J., Zhou,G., Dong,C., Zai,Y., Xu,W., Gao,F., Liu,M. and He,F.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1999) Department of Experimental Hematology, Institute of Radiation Medicine, Beijing Taiping Road 27, Beijing, Beijing 100850, P. R. China
FEATURES
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Location/Qualifiers
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BASE COUNT      800 a 638 c 556 g 577 t
ORIGIN

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Query Match      28.3%; Score 431.6; DB 11; Length 2571;
Best Local Similarity 59.6%; Pred. No. 1.3e-100;
Matches 728; Conservative 0; Mismatches 494; Indels 0; Gaps 0;

QY 298 TGTGTGGTAAAGTCCTGTGTTTCCCGAGTCAAGGCCATGGAACACCTCAAGCGCGACCGCG 357
DB 1143 TGCAGCGCTGTGCTGCCTGGTCCCTGCTCCCTGGCTGAGGATCCCAGGAGATGCTG 1202

QY 358 CTCAAAAAACCGACACCATCATCAGCACCAGACCATCCGACTTTTAAATAAATTACTC 417
DB 1203 CCCAGAAGACAGATACATCCCAACCATGATCAGGATCACCAACCTTCAACAAGATCACCC 1262

QY 418 CAAATTTAGCCGAATTTGCTTTTCTTGTATAGACAATTAGCTCATCAAAAGTAATCTA 477
DB 1263 CCAACCTGGCTGAGTTCGGCTTACGCCCATACCGCCAGCTGGCACACAGTCCACACGCA 1322

QY 478 CTAACATATTTTTTTAGTCTGTTTCTATTGGCACTGCTTTCCGCACTGTGAGTTTAGGTA 537
DB 1323 CCAATATCTTCTTCCCGAGTGGAGCATCGCTACAGCCCTTGTGCAATCTCTCCCTGGGA 1382

QY 538 CTAAGAGCCGATACCCATCAGCAGATTTTGAAGGTTTAACTTTAAATTTGACCGAAATCC 597
DB 1383 CCAAGCTGACACTCAGATGAATTCCTGGAGGGCCCTGAAATTTCAACCTCACGAGATTC 1442

QY 598 CAGAAGCCCAATTCACGAGGTTTTCAGAGATTGTTGAGAACCTTTCGAATCAACCTGATT 657
DB 1443 CGGAGGCTCAGATCCATGAAGCTTCCAGGAACCTCCTCCGTACCTCAACACCGACGACA 1502

QY 658 CTCATTTCAATTAACACTACTGTAACGGTTTATTTTGTCTGAAGGTTTAAAAATGGTTG 717
DB 1503 CCCAGCTCCAGCTGACCAACCGCAATGGCTGTTTCTCAGCGAGGGCTCAAGCTAGTG 1562

QY 718 ACAATTCCTAGAAGACGCTCAAGAACTATATCATAGTGAAGCTTTTACCGTTAATTG 777
DB 1563 ATAAGTTTTTGGAGATGTTTAAAAAGTTTACCACTCAGAGCTTTCACCTGTCAACTTCG 1622

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QY 838 AGATCGTTGACTAGTTTAAAGAATTAGATCGTATACCGCTTCGTCACCTAGTTAATACTA 897
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DB 1803 TCCACGTGGACAGGTGACACCGCTGAAGGTGCCTATGATGAAGCGTTTGGCATGTTTA 1862

QY 1018 ATATTCAACTTCACAAAAAATTAAGTTCTTGGTCTTATTAATGAAGTATTTAGTAACTAG 1077
DB 1863 ACATCCAGCACTGAAGAAGCTGCCAGCTGGGTGCTGCTGATGAATACCTTGGGCAATG 1922

QY 1078 CTACTGCTATTTTTTTTTTACCAGAGAGGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137
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QY 1018 ATATTCAACTTCACAAAAAATTAAGTTCTTGGTCTTATTAATGAAGTATTTAGTAACTAG 1077
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QY 1078 CTACTGCTATTTTTTTTTTACCAGAGAGGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137
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QY 1138 CTATGATCATATTACTAAATTTTTTAGAAGACGAGGATCGTGTAGCGCTTCTCTGCAACC 1197
Db 1983 CCCACGATATCATCAGCAAGTTCTCTGGAATAAGACAGAGAAGGTCTGCCAGCTTACATT 2042
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QY 1258 TTACCAAGTTTTTTTCTAACGGTGGCGATTTTGGTGGTGTACTGAGAGAAGCTCCATTAA 1317
Db 2103 TCACTAAGGTCTTTCAGCAATGGGCTGACCTCTCCGGGGTACACAGAGGAGCCCTGTA 2162
QY 1318 AATTGAGTAAAGCTGTTTCAAAAGCGCTTAACTATTATGATGATAAAGGTCACGAGGCGG 1377
Db 2163 AGCTCTCCAAAGCGGTCGATAGGCTGTGCTGACCATCGAGGAGAAAGGACTGAAGCTG 2222
QY 1378 CGGGCCTATGTTCTTGGAGCTATTCCAAATGAGCATTTCCACCAAGCTTAAATTTAATA 1437
Db 2223 CTGGGCCATGTTTTTAGAGGCCATATCCCATGTCTATCCCCCGGAGGTCAAGTTCACAA 2282
QY 1438 AACATTCGTTTTTCTGATGATCGAGCAGACACTAAAGCCCATTTGTTATGGGTAAAG 1497
Db 2283 AACCTTTGCTCTTAAATGATTGAACAAATAACCAAGTCTCCCTCTTTCATGGGAAAG 2342
QY 1498 TTGTCAACCCAACTCAGAAGTA 1519
Db 2343 TGGTGAATCCCAACCCCAANA 2364

RESULT 3
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LOCUS Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DEFINITION library, clone:0610011G14:serine protease inhibitor 1-4, full
insert, sequence.
ACCESSION AK002537
VERSION AK002537.1 GI:12832592
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA,
clone.lib:RIKEN full-length enriched mouse cDNA library
clone:0610011G14.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
JOURNAL MEDLINE 11042159
PUBMED 10349636
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
JOURNAL MEDLINE 11042159
PUBMED 10349636
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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Genome Res. 10 (11), 1757-1771 (2000)
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JOURNAL MEDLINE 11076861
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339 a 370 c 300 g 287 t
BASE COUNT
ORIGIN

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Db	170	CCATGAGATTGCTACAAACCTGGGAGACTTTGCCATCAGTCATACCGGAGCTGCTCCA	229		
QY	464	TCAAAGTAATTTACTAAACATTTTTTTTAGTCCGTGTTCTTANTGCCACTGCTTTCGCCAT	523		
Db	230	TCAGTCCAACACTTCCAACATCTCTTCGCCAGTGAGCATTTCCACAGCCTTTGCTAT	289		
QY	524	GTTGAGTTTATAGTACTAAAGCCGATACCCATCAGCAGATTTTCAAGGTTTAAACTTTAA	583		
Db	290	GCTCTCCCTAGGAGCAAGGTTGACACTCACACGCGAGTCTCAGGGCCTCGAGTTCAA	349		
QY	584	TTTCACGCCAAATCCCAAGAGCCCAATTCACGAGGGTTTTCAAGAGTGTGTGAGAACTTT	643		
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Db	530	CTCTGTCACTTTGCGAGAGTCAGAGGAGGCCAAGAAGTGATTAATGATTTTGTGGAGAA	589		
QY	824	AGGCACCCAGGGTAAGATCGTTTGACCTAGTTAAAGAAATTAGATTCGTCTTCGCG	883		
Db	590	GGGAACCCAGGAAGATAGTTGAGGCTGTGAAATAAATCTAGAACAGACACAGTTTCGT	649		
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Db	650	CTTGGCAATTAATCTCTTTAAAGGCCAATGGAAGAAGCCATTCGATCCTTGGAACAC	709		
QY	944	TGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAGTTTCCAATCATGAAAG	1003		

Db	710	TAAGCAAGCTGAGTTCACAGTGGACGAGTCCACACAGGTAAGGTGCCCATGATGACCTT	769
QY	1004	ACNCGGTATGTTCAATATTCACATTTGCAAAAAATAAGTTCCTTGGCTTTAATTAAGAA	1063
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QY	1064	GTATTTAGGTAACGCTACTGCTATTTTTTTTTTACCAGCAAGGTAAGCTTCAACATTT	1123
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QY	1124	AGAGAATGAGTTGACTCATGACATTAATTACTTAAATTTTTTACAGAACGAGGATCGTCGTAG	1183
Db	890	GGAGCAAACTCTCAACGAAGGAGCTCATCTCAAGTTCCTGCTTAACAGGCCGACAAGTT	949
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QY	1361	MAAGGGTACCAGGCCCGCGCGCTATGTTCTTGGAAAGCTATTCCAATGAGCATTCACC	1420
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QY	1421	AGAAGTTAAATTTAATAACCATTCGTTTTTCTTGATGTCGAGCAACACTTAAAGCCC	1480
Db	1190	TATCTTGCACTTCAACGCGCCTTCTCTTTTCTCATTAATTTTGAAGACACTCTCAGAGCC	1249
QY	1481	ATTGTTTTATGGTAAAGTTGTCAACCCCAACTCAGAAGT	1518
		1250	

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RESULT 5
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DEFINITION
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    887 bp mRNA linear EST 15-JUL-2002
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    5', mRNA sequence.
ACCESSION
    BQ643710
    BQ643710.1 GI:21767882
KEYWORDS
    EST.
SOURCE
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ORGANISM
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    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
    1 (bases 1 to 887)
    NIH-MGC http://mgc.nci.nih.gov/.
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Strausberg, Ph.D.
    Email: cgapbs-re@mail.nih.gov
    Tissue Procurement: CGAP (Stanford)
    CDNA Library Preparation: Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    plate: LICM2439 row: n column: 02
    High quality sequence stop: 731.
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    Location/Qualifiers
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EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      242 a      224 c      232 g      187 t      2 others
ORIGIN

Query Match
Best Local Similarity 20.3%; Score 309.8; DB 14; Length 887;
Matches 532; Conservative 0; Mismatches 354; Indels 1; Gaps 1;

QY 519 GCATGTTGAGTTAGTTAGTAAAGCCGATACCCATGACGAGATTTTGAAGGTTTAAAC 578
Db 1 GCAATGCTCTCCCTGGGACCAAGCTGACACTCACCATGAATCTCGGAGGCCTGAAT 60
QY 579 TTTAATTTGACCGAAATCCCAAGACCCCAATTCACAGAGGTTTCAAGAGTTGTTGAGA 638
Db 61 TTCAACCTCAGGAGATTTCCGGAGGCTCAGATCATGAAGGCTTCAGGAACCTCCCTCGT 120
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Db 121 ACCCTCAACGACGACAGCCAGCTCCAGCTGACCCACCGCAATGGCTGTTCTTCACG 180
QY 699 CAAGGTTTAAATTTGGTTTGACAAATTCCTGAAGACGCTCAAGAAACTATATCATGTAG 758
Db 181 GAGGCGCTGAAGCTAGTGGATAAGTTTGTGAGGATGTTAAAAAGTTGTACCACTCAGAA 240
QY 759 GCTTTTACCGTTAATTTTGGTGATCTAGTGGAGAGCTTAAAGCAATTAATGATGTT 818
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QY 939 GATACTGAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCAAAAGTTCCAAATGATG 998
Db 421 GACACCGAGGAAGAGGACTTCCAGCTGGACAGGTGACCACCGTGAAGTGCCTATGATG 480
QY 999 AAAGAGCTGGGTATGTTCAATTTCAACATTCGAAATTAAGTTCTTGGGTCTTATTA 1058
Db 481 AAGCGTTTAGCGATGTTTAACTCCAGCACTGAAGAAGCTGTCAGCTGGGTGCTGCTG 540
QY 1059 ATCAAGTATTTAGTTAACTGCTACTGCTATTTTTTTTTTACCAGCAAGGTAAAGCTTCAA 1118
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QY 1119 CATTTAGAGAATGAGTTGACTCATCATATTTACTAATATTTTGAAGAAGGAGATCGT 1178
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QY 1179 CGTAGCGCTTCTGCACCTGCAAGTTAAAGTATCACCGGTACTTACGACTTAAATCT 1238
Db 661 AGGTCTGCGAGCTTACATTTTACCCAACTGTCCTTACTGAACTATGATCTGAAGAGC 720
QY 1239 GTTTTAGGCCAGTTAGTATTTACCAAGTTTTCCTAACGGTGCCTGTTGAGTGGTGT 1298
Db 721 GTCCTGNGTCACTGGGATCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGNGTC 780
QY 1299 ACTGAAGAGCTTCCATTTAAATTTGAGTAAAGCTGTTTCAAGAGCCGCTTAACTATGAT 1358
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Db 840 GAGAAAGGAGCTGAAGCTGCTGGGCCATGTTTTTTAGAGGCCATACC 886

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LOCUS
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AGENCOURT_8351269 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6286839
5', mRNA sequence.
B0648909
B0648909.1 GI:21773081
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 907)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2488 row: e column: 16
High quality sequence stop: 721.
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/db_xref="taxon:9606"
/clone="IMAGE:6286839"
/tissue_type="NIH_MGC_100"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT      246 a      228 c      239 g      192 t      2 others
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Query Match
Best Local Similarity 20.0%; Score 305.4; DB 14; Length 907;
Matches 530; Conservative 0; Mismatches 356; Indels 1; Gaps 1;

QY 541 AAGCCGATACCCATGACGAGATTTTAGAAGGTTTAACTTTAACTTTGACCGAAATCCAG 600
Db 15 AGCTTGACACTCCGATGAATCTCGGAGGCGCTGAATTTCAACCTCAGGAGATTCGG 74
QY 601 AAGCCCAATTCACGAGGTTTTCAGAGAGTTGTTGAGAACTTTCGAATCAACCTGATTC 660
Db 75 AGGCTCAGATCCATGAAGGCTTCCAGGAACCTCCCGTACCTCAGCAGCAGCAGCC 134
QY 661 AATTCGAATTAACACTACTGTAACGGTTATTTTGTCTGAAGGTTTAAATTTGTTGACA 720
Db 135 ACTCCAGCTGACCAACCGGCAATGCGCTGTTCCTCAGCGAGGCGCTCAAGCTAGTGA 194
QY 721 AATTCCTAGAAGACGCTCAAGAACTATATCATAGTAGGCTTTTACCGTTAAATTTGGTG 780
Db 195 AGTTTTTGAGGATGTTTAAAAAGTTGTACCACTCAGAAAGCTTCACCTGCACTTCCGGG 254
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Db 777 ACATCCAGCAGCTGTAAGAAGCTGCCAGCTGGTCTGCTGATGAATACCTGGGGCATG 836
 QY 1078 CTACTGCTATTTTTTTTACAGACGAGAGGTAAAGCTTCAACATTTAGAGAA 1129
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RESULT 8
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 DEFINITION 5', mRNA sequence.
 ACCESSION BM924019
 VERSION BM924019.1 GI:19374398
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 985)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL2806 row: m column: 16
 High quality sequence stop: 707.
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 /clone="IMAGE:5760183"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dr primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH_MGC Library."
 BASE COUNT 258 a 270 c 242 g 213 t 2 Others
 ORIGIN

Query Match 18.8%; Score 287; DB 14; Length 985;
 Best Local Similarity 59.5%; Pred. No. 2.6e-63;
 Matches 519; Conservative 0; Mismatches 351; Indels 2; Gaps 2;

QY 298 TGTGTGTAAGTCCGTGTTTCCCGAGTCAAGGCGATGGAAGACCTCAAGCGACGCG 357
 Db 54 TGCAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 113
 QY 358 CTCAAAAACCCAGACAGTATACACGACCAAGACCATCCGACATTTAATAAATTA 417
 Db 114 CCAGAGACATATATCCACCATGATCAGGATCACCCAACTTCAACAGATCACCC 173
 QY 418 CAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAAATAGCTCATCAAGTAATCTA 477
 Db 174 CCAAGCTGGCTGAGTTCGCTTACCGCTATATACCGGAGCTGGACACAGCTCAACAGCA 233
 QY 478 CTAACATTTTATAGTCTGTTCTATTGCGCACTGCTTTGCGCAAGTTAGGTA 537

Db 234 CCAATATCTCTCTCCCCAGTGAGCATCGCTACAGCCCTTGGCAATGCTCTCCCTGGGGA 293
 QY 538 CTAAGCCGATACCCATGACGAGATTTTGAAGGTTTAAACTTTAAATTTGACCCAAATCC 597
 Db 294 CCAAGGCTGACACTCAGCATGAATCCCTGGAGGGGCTGAATTTCAACCTCAGCGAGATTC 353
 QY 598 CAGAAAGCCCAATTCACGAGGTTTTCAGAGATTTTTCAGAACCTTTGANTCAACCTGATT 657
 Db 354 CGAGGCTCAGATCCATGAAGCTTCCAGGAACCTCCCGTACCTCAACAGCCAGACA 413
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 Db 474 ATAAGTTTTCGAGATGTTTAAAGTTGTACCACTCAGAAAGCTTTCACCTGTCAACTTCG 533
 QY 778 GTGATCTAGGAAAGCTAAAAGCAAAATTAATGATTTATTTGAGAAAGGACCCAGGTA 837
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 QY 838 AGATCGTTGACCTAGTTAAAGAAATTAGATCGTATACCGCTTTCGCACCTAGTTAACTATA 897
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 Db 714 TCCAGTGGACAGGTGACCAAGCTGTAAGGTCCTATGATGAAGCTTTAGGCATGTTTA 773
 QY 1018 ATATTCACATTTGCAAAAAATTAAGTTCTTGGGCTTTATTAATGAAGTATTAGTAAAG 1077
 Db 774 ACATCCAGCACTCTAAGAGCTGTTCCAGCTGGGTGCTGCTGATGAATACCTGGGCAATG 833
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 Db 834 CCACCGCCATCTCTCTTCNTGGCTGATGAGGGGAACTACAGGCACTGGAATAATCACTC 893
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 Db 894 AC-CAGATATCATCAAGGTTCTCGGAAA 924

RESULT 9
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 BQ646142.1 GI:21770314
 VERSION
 BQ646142.1
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 982)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCN2504 row: a column: 14

Mon Dec 9 12:50:59 2002

High quality sequence stop: 647.

Location/Qualifiers

source

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/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 267 a 238 g 217 t 1 others
ORIGIN
Query Match 18.7%; Score 285.2; DB 14; Length 982;
Best Local Similarity 59.8%; Pred. No. 7.6e-63;
Matches 496; Conservative 0; Mismatches 333; Indels 1; Gaps 1;
QY 627 GAGTGTTCGAGAACTTGAATCAACTGATCTCAATTTGCAATTAATCACTACTGTGTAACGGT 686
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QY 687 TTATTTTGTCTGAAGTTTAAATTTGGTTGACAAATTCCTPAGAGAGCTCAAGAACTA 746
Db 61 CTGTTCTCAGCGGCGCTGAAGTAGTGGATAAGTTTGGAGGATGTTAAAGATTG 120
QY 747 TATCATAGTGAAGCTTTACCGTTTAATTTTGTGTACTAGTGGAGCTAAAGCAAAAT 806
Db 121 TACCACATCAAGACCTTCACTGTCACTTCGGGGACACGAGAGCGCCAAACAGATC 180
QY 807 AATGATATGTTTCAGAAAGCCACCCAGGTAAGATCGTTTGACCTAGTTTAAAGAAAT 866
Db 181 AAGCATGTTAGTGAGAGAGGTTACTCAAGGAAATTTGTGATTTGTTCAAGGAGCTTGC 240
QY 867 CGTATACCTCTTCGACATGATTAATTTTTCAGGGTAAGTGGGAAGCTCT 926
Db 241 AGACACAGCTTTTGTCTGTGTAATACATCTCTTTAAAGGCAATGGGAGAGACC 300
QY 927 TTCAGGTTAAGATCACTGAAGAGGAATTTTCATGTTGATCAAGTTACTACTGTCAA 986
Db 301 TTTGAAGTCAAGGACACCCGAGAGAGGACTTCCACGTGGACAGGTGACACCGGTGA 360
QY 987 GTTCCAATGATGAAAGAGCTGGGTATGTTTCAATTTCAACATTCGCAAAATTAAGTTCT 1046
Db 361 GTGCTATGATGAAGCGTTTGAAGCATGTTTAAATCCAGCATGTAAGAGCTGTCCAGC 420
QY 1047 TGGGTCTTATTAAGTATTTAGTGAAGCTGCTGCTATTTTTCCTGCTGCTGATGAG 1106
Db 421 TGGGTGCTGCTGATGAATACCTGGGCAATGCCACCGCATCTTCTGCTGCTGATGAG 480
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Db 481 GGGAACTACAGCACCTGGAAATGAATCAACCCAGCATATCATCAAGTTTCTTGGAA 540
QY 1167 AACGAGGATGCTGTAGCGCTTCTGCACTGCGCAAGTTTAAGTATCAACCGTACTTAC 1226
Db 541 AATGAAGACAGAAAGTCTGCCAGCTTACATTTTACCAGAACTGTCATTTACTGGAACCTAT 600
QY 1227 GACTTAAATCTGTTTTAGGCGAGTATAGTATTTACCAAGT- TTTTCTTACGCTGCCGA 1285
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QY 1286 TTTGAGTGTGTTTACTGAAGAGCTCCATTAATTTAGTAAAGCTGTTCACAAAGCGGT 1345
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QY 1346 CTTAACTATTGATGAAAAGGTTACCGAGCGCGGCTATGTTCTTGGAGCTATTTC 1405
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QY 1406 AATGAGCATTCACACGAGTAAATTTAATAAACATTCGTTTTTCTGTA 1455
Db 781 CATGCTATCCCCCGGAGGCGAGTTCAACCAACCCCTTGTCTCTTCTTA 830

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5', mRNA sequence.
BO958958
BO958958.1 GI:22374436
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 924)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L102667 row: k column: 18
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Location/Qualifiers
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/notes="Organ: prostate; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 251 a 253 c 226 g 193 t 1 others
ORIGIN
Query Match 18.6%; Score 283.8; DB 14; Length 924;
Best Local Similarity 58.4%; Pred. No. 1.7e-62;
Matches 513; Conservative 0; Mismatches 363; Indels 2; Gaps 1;
QY 408 AAAATTTACTCCAAATTTAGCGGAATTTGCTTTTCTTTGATATAGACAATTAGCTCATCAA 467
Db 2 AAGATCACCCCAACCTGGCTGAGTTTCGCTTCAGCCTATACCCGACGCTGGCACACAG 61
QY 468 AGTAATTTCTACTAACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 527
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QY 528 AGTTTAGGTACTTAAGCCGATACCCATGACAGATTTTGAAGGTTTAACTTTAATTTG 587
Db 122 TCCCTGGGACCAAGGCTGACACTCACGATGAAATCTCGGAGGCGCTGAATTTCAACCTC 181
QY 588 ACCGAAATCCAGAGACCCCAATTCACGAGGTTTTCAGAGAGTTTGTGAGAACTTTGAAT 647

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QY	708	AAATTTGGTTGACAAATTCCTAGAACGCTCAAGAACTATATCATAGTAGGCGCTTTTACC	767
Db	302	AACCTAGTGATGATTTTGGAGATGTTAAAAAGTTTAAACCTCAAGAGCCCTTCACT	361
QY	768	GTTAATTTGGTGATCTACTGAGGAAGCTAAAAAGCAAAATTAATGATTATGTTGAGAAAGGC	827
Db	362	GTCAACTTCGGGACACCGCAAGAGCCAAAGAACAGATCAACGATTAGCTGCGAAGGCT	421
QY	828	ACCCAGGGTAAGATCGTTGACCTAGTTAAAGAAATTAAGATCGTGATACCGCTTTCGCACTA	887
Db	422	ACTCAAGGAAATTTGTGATTTGCTCAAGGAGCTTTGACAGAGACACAGTTTTCCTCTG	481
QY	888	GTTAACTATATTTTTCAGGGTAAGTGGGAAGCTCTCTTTCGAGGTTAAAGATACATGAA	947
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QY	948	GAGGAAGATTTTTCATGTTGATCAAGTTACTACTGTCAAAAGTTCCAAATGATGAAGAACTG	1007
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Db	722	AATGAATCAACCCAGGATATCATCAGCTGTCAGCTGGGTGCTGATGAAGATAC	781
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Db	782	CCACTTACATTTTACCCAACTGTCCATTTACTGGAATATGATCTGAAGAGGCTCTCG	841
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RESULT 11			
BM924813			
LOCUS			
DEFINITION	BM924813	1194 bp mRNA linear EST 12-MAR-2002	
ACCESSION	AGENCOURT_5653921	NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5761267	
VERSION	BM924813	5', mRNA sequence.	
KEYWORDS	BM924813.1	GI:19375192	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	NIH-MGC (bases 1 to 1194)		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)		
	Clone distribution: MGC clone distribution Information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM12809 row: j column: 20		

FEATURES	High quality sequence stop: 662.		
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	/clone_lib="NIH_MGC_116"		
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	/note="Organ: pooled colon, kidney, stomach; Vector: PCMV-SPT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."		
BASE COUNT	321 a 303 c 328 g 242 t		
ORIGIN			
	Query Match	18.0%; Score 274.8; DB 14; Length 1194;	
	Best Local Similarity	61.2%; Pred. No. 4e-60;	
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QY	832	AGGTAAGATCGTTGACCTAGTTAAAGAAATTAAGTATCGTATACCGCTTTCGCACTAGTTA	891
Db	67	AAGGAAAAATTTGTGATTTGCTCAAGGAGCTTGACAGAGACACAGTTTTCCTCTGGTGA	126
QY	892	ACTATATTTTTTCAAGGGTAAGTGGCAAGCTCTTTCGAGGTTAAAGTACTGGAAGAGG	951
Db	127	ATTACATCTCTTTAAGGCAATGGGAGAGACCCCTTTGAAGTCAAGGACACCGGAAAG	186
QY	952	AAGATTTTCATGTTGATCAAGTTACTACTGTCAAAGTTTCAATGATGAAGAACTGGGTA	1011
Db	187	AGSACTTCCACGTGGACCAAGTGACCACTGAAAGTGGCTATGATGAGCGTTTAGGCA	246
QY	1012	TGTTCAATATTCACATTCGCAAAATTAAGTCTTGGGTCTTTAATGAAGTATTTAG	1071
Db	247	TGTTAATCCAGCACTGTAAAGAGCTGTCCAGCTGGGTGCTGTGATGAATACCTGG	306
QY	1072	GTAACGCTACTGCTATTTTTTTTTTACCAGCAAGGTAAGCTTCAACATTTAGAGAAATG	1131
Db	307	GCAATGCCACCGCATCTTCTCTCTGCTGATGAGGGGAACTACAGCACTTGGAAATG	366
QY	1132	AGTTGACTCATGACATTTACTTAAATTTTATAGAACAGGATCGTCTAGCGCTTCTC	1191
Db	367	AATCAACCCACGATATCATCAAGTTCTCTGGAATTAAGGCTGTGATGAGAGCGCTC	426
QY	1192	TGCACCTGCCCCAAAGTTAAGTATCACCGGTACTTACGACTTAAATCTGTTTAGGCCAGT	1251
Db	427	TACATTTACCAAACTGCTCCATTTACTGGAACCTATGATCTGAAGAGCGCTCTGGTCAAC	486
QY	1252	TAGGTATTTACCAAGTTTTTTTCTAACGGTGGCGATTTGAGTGGTGTACTGAAGAGCTC	1311
Db	487	TGGGCATCACTAAGGTCTTTCAGCAATGGGCTGACCTCTCCGGGTACACAGAGGCGAC	546
QY	1312	CATTAATAATTTAGTAAAGCTGTTCAAAAGCGCTTTAACTATTGATGAAGAGGTTACCG	1371
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QY	1372	AGGCCCGCGGCTATGTTCTCTGGAAGCTATTCCAACTGAGCATTTCCACCAAGCTTAAT	1431
Db	607	AAGCTGCTGGGCGCATGTTTTTAGAGGCCATACCCATGCTATCCCCCGGAGTCAAGT	666
QY	1432	TTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAAAAGCCCACTTTGTTATGG	1491
Db	667	TCAACAAACCCCTTTGCTTCTTAATGATTGAACAAATACCAAGTCTCCCCCTCTCATGG	726

Mon Dec 9 12:50:59 2002

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QY 1492 GTAAGG 1497
Db 727 GAAAG 732

RESULT 12
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AGENCOURT_8298326 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6269613
5', mRNA sequence.
ACCESSION BQ650189
VERSION BQ650189.1 GI:21774361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 907)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Location/Qualifiers
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/notes="Organ: liver; Vector: pOTB7; Site: 1; XhoI; Site 2:
ECORI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 245 a 237 c 226 g 198 t 1 others
ORIGIN
Query Match 17.9%; Score 273.4; DB 14; Length 907;
Best Local Similarity 59.4%; Pred. No. 8.4e-60;
Matches 498; Conservative 0; Mismatches 337; Indels 3; Gaps 2;

QY 660 CAATTGCAATTAACCTACCTGGTAAACGGTTATTTTGTCTGAAGTTTAAATTTGGTTGAC 719
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QY 720 AAATTCCTAGAGAGCTCAAGAACTATATCATAGTAGGCTTTTACCGTTAATTTTGGT 779
Db 67 AAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAAGGCTTCACCTGTCACCTCGGG 126

QY 780 GATACGAGGAGCTTAAAGCAATTAATGATTATGTTGAGAAAGGCAAGGCGGTAAG 839
Db 127 GACACGGAAGAGGCGCAAGAAACAGATCAACGATTACGTGGAGAGGGTACTCAAGGAAA 186

QY 840 ATCGTTGACCTAGTTAAAGAAATTAGATCGTGATACCGCTCTTCGCGACTAGTTAATATTT 899
Db 187 ATTTGTTGATTTGTCAGGAGGCTTGACAGAGACACAGTTTTTGTCTGTGTTGATATCATC 246

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Mon Dec 9 12:50:59 2002

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QY 900 TTTTCAAGGGTAAGTGGGAACGCTCTTTTGGAGGTTAAAGATACCTGAAGAGCAAGATTTT 959
Db 247 TTTTCAAGGGTAAGTGGGAACGCTCTTTTGGAGGTTAAAGATACCTGAAGAGCAAGATTTT 306

QY 960 CATGTTGATCAAGTTACTACTGTCAAAAGTTCCTCAATGATGAAAGAGACTGGGTATGTTCAAT 1019
Db 307 CACGTGGACCAAGTGCACCGTGAAGTGCCTATGATGAAGCGTTTAGGCATGTTTAAAC 366

QY 1020 ATTCAACATTCGAAAAAATTAAAGTTCCTTTGGTCTTATTAATGAAGTATTAGCTAAGCT 1079
Db 367 ATCCAGCACTTAAGAAAGCTGCTCCAGCTGGTGTGCTGATGAATAATACCTGGGCAATGCC 426

QY 1080 ACTGCTATTTTTTTTACCAGACGAAAGGTAAGCTTCAACATTTAGAGAATAGTGTGACT 1139
Db 427 ACCGCCATCTTCTTCTGCTGATGAGGGGAACTACAGCACCTGGGAAATGAATCACTCACC 486

QY 1140 CATGACATTTACTATAAATTTTATAGAGAACGAGGATCGTGTAGCGCTTCTTCGACCTG 1199
Db 487 CAGATATCATCACAAGCTTCTTGAAATGAAGACAGAGGCTGCGCAGCTTACATTTA 546

QY 1200 CCAAGTTAAGTATCACCGGTACTTACGACTTAAATCTGTTTGTAGCCAGTTAGGTATT 1259
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QY 1260 ACCAAGTTTTTCTAAGCGTGCCGATTTGAGTGGTGTGTTACTGAAGAGCTTCCATTTAAA 1319
Db 607 ACTAAGTCTTCAGCAATGGGCTGACCTCTCCGNGTCAAGAGAGGAGGCCACCTGAAG 666

QY 1320 TTGAGTAAAGCTGTTTCAAAAGCGCTCTTAATGATGAAAGGTTACCGAGCGGCC 1379
Db 667 CTCTCAAGCGCTGCTAAGGCTGTCTGACCATCGAGGAGAGG-ACGTGAACCTGCT 725

QY 1380 GCGCTATGTTCTGGAAGCTATTCCATGAGCATTCCACCAGAGTTAAATTTAA--TA 1437
Db 726 GGAGCCATGTTTTTAGAGGCGCTACCCATGCTCTATCCCCCCCCCGAGTCAAGGTTACCAA 785

QY 1438 AACCATTCGTTTTCTGATGATCGAGCAGACACATAAAGCCCATGTTATGGGTAA 1495
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RESULT 13
BQ646948 891 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8302495 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6271313
5', mRNA sequence.
ACCESSION BQ646948
VERSION BQ646948.1 GI:21771120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 891)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2447 row: n column: 18
High quality sequence stop: 672.
Location/Qualifiers
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Sf11 (ggccgctcgcc); Site_2: Sf11 (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCATAGCCGCGAGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

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QY	439	TTTCTTTGTATAGACAAATTAGCTCATCAAAATTAATCTTACTAACAATTTTTTTAGTCTG	498		
DB	61	TCAGCCTATACGCCACGCTGGCACACCACTGTCACAGACCAATATCTCTCTCCCCAG	120		
QY	499	TTTCTATTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACG	558		
DB	121	TGAGCATCTGCTACAGCCTTTGCAATCTCTCTCTGGGACCAAGCTGACACTCAGATG	180		
QY	559	AGATTTTAGAAGGCTTTAAACTTTTAAATTTGACCGAAATCCAGAACCCCAATTCACGAGG	618		
DB	181	AAATCTGGAGGCTTGAATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAAG	240		
QY	619	GTTCCTAAGAGTTGTTGAGAACCTTTGAATCAACCTGATTTCAATTTGCAATTTAACTACTG	678		
DB	241	GCTTCCAGGAACCTCCCTCATATACCTCAACAGCCAGACAGCCAGCTCCAGCTGACCAAG	300		
QY	679	GTAACGCTTTTATTTGCTGTAAGGCTTTAAATTTGTTGACAAATTTCTTAGAAGAGCTCA	738		
DB	301	GCAATGGCTTTCTCTCAGCGAGGCTGAAAGCTAGTGGATAGTTTNTGGAGGATGTA	360		
QY	739	AGAACTATATCATAGTAGGAGCTTTTACCGTTAATTTTGTGTGATCTAGGAGGCTTAAAT	798		
DB	361	AAAAATTTGTACACTCAGAACGCTTCACTGTCAACTTCGGGGACACCGAGAGGCCAAGA	420		
QY	799	AGCAATTAATGATTATGTTGAGAAAGCCACCCAGGCTAAGATCTGTGACCTTAGTTAAAG	858		
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QY	859	AATTAGATCTGTATACCGCTCTTCGCATAGTTAACTATATTTTTTTCAAGGGTAACTGGG	918		
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DB	600	CCGTGAAGTGCCATATGATGAAGGCTTTAGCATGTTTAACTATCCAGCTGTAAGAAGC	659		
QY	1039	TAAATTTCTGGTCTTATTAATGAAGTATTTAGTCAAGCTACTGCTATTTTTTTTAC	1098		
DB	660	TGTCACAGCTGGGTGCTGTGATGAATACCTGGGCAATGGCACCGCAGCTCTTCTCTGC	719		
QY	1099	CAGACGAGGTAAGCTTCAACATTTTAGAGAAATGAGTTGACTCATGACATTTACTAAAT	1158		
DB	720	CTGATGAGGGGAATTTACAGCACCCTGGAAACATGAATCAACCA-GATATCATCACCAAGT	778		
QY	1159	TTTTAGAGAACGAGGATC	1176		
DB	779	TCTTGGAAAACTGAGACC	796		

QY	810	GATTATGTTGAGAAAGCACCAGGTAAGATCGTTGACCTAGTTAAAGAAATTAGATCGT	869
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QY	870	GATACCGCTTCCGCACTAGTTAACTATATTTTTTCAAGGTAAGTGGGAACGTCCTTTTC	929
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QY	930	GAGGTTAAAGATCACTCAAGAGCAAGATTTTCATGTTGATCAAGTTACTGTTCAAAAGTT	989
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QY	990	CCAATGATGAAAGACTGGGTATGTTCAATATTAACATTCGAAAAAATTAAGTCTTTGG	1049
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DB	721	CTGAAGAGGCTCTGGTCACTAGGCACTACTAAGGGCTTCAGCCATGGGCTGGACT	780
QY	1289	GAGTGGTGTACTGAAGAGCTCC	1312
DB	781	CCCCGGGGTTCACAGAGGAACGCC	804
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ACCESSION	BS567260		
VERSION	BS567260.1	GI:13574913	
KEYWORDS	EST.		
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ORGANISM	Homo sapiens		
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AUTHORS	1. (bases 1 to 796)		
TITLE	NIH-MGC http://mgi.nci.nih.gov/ .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: CLONETECH Laboratories, Inc. cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LCM1583 row: b column: 11 High quality sequence stop: 730.		
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Mon Dec 9 12:50:59 2002

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Search completed: December 6, 2002, 23:32:54
Job time : 1546.5 secs

